

1 GCTGTGGAA CCTCTCCACG CGCAGCAACT CAGCCAAACGA TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC  
CGACACCCCTT GGAGAGGTGC GCGTGTCTGA GTCTGTCTGA AAAGACTATC TAAAAACCCCT CAAACTGGTC TCTACGTTCC CCACCTCCTC GCGAAAGGAG

101 CGTTAGGAA CTCTGGGGAC AGAGCGCCCC GCGCGCCTGA TGGCCGAGGC AGGTGCGAC CCAGGACCCA GAGCGCGTC GGAACCATTA CCATGGCCCC  
GCAATCCCTT GAGACCCCTG TCTCGCGGG TCTCGCGGACT CCGCGGACT ACCGGCTCG TCCACGCTG GGTCTGGGT CCTTGGGTAT GTACCGGCG  
MetalArg

201 GATCCCCAAG ACCCTAAAGT TCGTCTCGT TCGTCTCGT CATCTGCTGC GTCTGCTGC CAGTCTCTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG  
CTAGGGGTTT TGGGATTCA AGCAGCAGCA GTAGCAGCG CAGGACGAC GTACGATCG ATGAGACGG TGGTACGGG CCGTCTCCT TCAAGGGGTC

4 IleProlys ThrLeuLysP heValValVa lileValala ValLeuLeup roValLeuAl aTySerAla ThrThrAlaa rGlnGluGl uValProGln

301 CAGACAGTGG CCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGT TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCGGTGCA  
GTCTGTACC GGGGTCTCGT TGTCTCCGT TCGAAGTTC TCGAAGTTC CCTCTCAC AGTCTGCTT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT

37 GlnThrVala laProGlnG lGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

401 CAGAGGGTGT GGAATACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT  
GTCTCCACA CCTAATGTGG TTGCGAAGGT TGTACTTGG AAGAACAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA

71 GluGlyVa lAspTyThr AsnAlaSerA sNasngluPr oSerCysPhe ProCysThrv aLcysLysse rAspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTCCCG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC  
CTGGTCTCTG TGTACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTACATCGT CCACGGGATC ACCCTTCAG

104 ThrArgasp ThrValCysG lnCysLysG lileGlnCysv algluGluph eGlyAlaasn AlaThrValG luthrProAl aalagluGl uThrMetAsnThr

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAAT TTGTCGCAAT GCCACTGTGG AAACCCACAG TGTGAAGAG ACAATGAACA  
GTTTCACTAT TAACATGAC GACCTACTA TAGGTACAC ACTTCTTAA ACCACGGTTA CCGTGACACC TTTGGGTCG ACGACTTCTC TGTACTTGT

137 GlnValSerA snCysThrSe rTrpAspasp lileGlnCysv algluGluph eGlyAlaasn AlaThrValG luthrProAl aalagluGl uThrMetAsnThr

701 CCAGCCCGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG  
GGTCGGGCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGTGTCG GTCCCTGAG GACGGGTG CCGACTTCTC TGTACTGTT hrSerProGly

171 SerProG lYthrProAla ProAlaAlag luGluThrMe tAsnThrSer ProGlyThrp roAlaProAl aalagluGl uThrMetThrt hrSerProGly

801 GACTCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCTGCC  
CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGTGTCG GCGCCCTGAG GACGGGTG CCGACTTCTC TGTACTGTT hrSerProGly

204 ThrProAla ProAlaAlag luGluThrMe tThrThrser ProGlyThrp roAlaProAl aalagluGl uThrMetThrt hrSerProG lYthrProAla

901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTTTTTTTTTT GAAAGACTTC ACTGTGGAAG AAATTCCTTC  
AGAAAGATAA TGGAGAGTAC GTGGTAGCAT CCTAGTATC AAGATTAA CA GAAGACTAA CACAAAACAAA CTTTCTGAG TGACACTTC TTTAAGGAAG

237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIlev alLeuIleVal ValPheVal

1001 CTTACCTGAA AGGTTACAGT AGGCGTGGC TGAGGGCGGG GGGCGTGG CACTCTGTC CTTGCTGTGT TCCACAGAC AGAAACGCTT  
GAATGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGGCC CCGCGGACCT GTGAGAGAC GGACGGAGG AGACGACACA AGGTGTCTG TCTTTGGGA

1101 GCCCTGCC CAAAAA  
CGGGACGG GTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

[illegible]

Apo2	1	-----MEQRGONAPAASGARKRHGPGPREARGARPGLRVPKTLVL
Apo2DcR	1	-----MARIPKTLKFVV
DR4	51	GRGALPTSMGQHGPSARARAGRAGPEPAREASPRLRVHKTFFKFVVVGVL
Apo2	41	VVAAVLLLVSAESALITQODLAPQORAAPOOKFSSPSEGLCPFGHHISED
Apo2DcR	13	VIVAVLLPVLAYSATTARQEEVPOOTVAPOQORHSFKGEECFAGSHRSEH
DR4	101	LQVVPSSAATIK-----LHDQSIGTQOWEHSPLGELCPFGSHRSEH
		CRD1
Apo2	91	GRDCISCKYGQDYSTHWNDLLFCLRCTREDSCGEVELSPCTTTTNTVCOCE
Apo2DcR	63	TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTTDTVCOCK
DR4	142	PGACNRCTEGVGYNASNLLFACLPCCTACKSDEEERSPCTTTTNTACOCK
		CRD2
Apo2	141	EGTFREEDSPERMCRKCRFGCPGCMVKVGDCTPWSDIKCVHKE-----
Apo2DcR	113	EGTFERNENSPERMCRKCSR-CESGEVQVSNCTSWDDIQCV-EFGANATVE
DR4	192	PGTFERNENSAEMCRKCRSTGCPGCMVKVKDCTPWSDIKCVHKE-----
Apo2		-----
Apo2DcR	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4		-----
Apo2	183	-----SGTIIGVTVAAVVLLVAVFV---
Apo2DcR	211	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
DR4	234	-----SNGHNIWVVLVVLVPLIVAV-LIVC
Apo2	203	CKSLLWKKVLPYLKGICSGGGGDPEVDRSSQRPGEADNVLNEIVSILQP
DR4	262	CCIGSGCGGDEKCMMDRVCFWRLGLLGPGEADNAHNEILSNADSLSTFVS
Apo2	253	TQVPEQEMEVOEPAEPTGVNMLSPGESEHLLPAAEAERSORRRLLVPANE
DR4	312	----EQOMESOEPAIDLTVTVQSPGEAQCLLGPAAEAGSORRRLLVPANG
Apo2	303	GDPTETLRQCFDDFADLVPPDSWEPLMRKLGMDNEIKVAKAEAAGH--R
DR4	358	ADPTETLMLFFDKFANIVPPDSWDQMLRQDLTKNEIDVVRAGTAGP--G
Apo3/DR3	338	VMDAVPARRWKEFVRTLGREAEIEAVEVEI-GRF-R
TNFR1	322	VVENVPLRWKEFVRRIGLSDEHIDRLLELON-GRCLR
CD95	220	IAGVHTLSQVKGFVREKNGVNEAKIDEIKNDN-VQDTA
Apo2	351	*DTLYTMLIKVVKTKGR-DASVHTLLDALETIGERLAKOKIEDHLLSSGKF
DR4	406	DALYAMLMKVVNKTKGR-NASHTLLDALERMEERHAKKEIODLLVDSGKF
Apo3/DR3	374	DQOYEMLKRWRQOQP---AGLGAVYAALERMGLDGCVEDLRS
TNFR1	358	EAQYSMLATWRRRTTPREATLELLGRVLRDMDLLCLEDIEE
CD95	256	EQKVQLERNWHQLHGKKEAY-DTLIKDLKKANLCTLAEKIQT
Apo2	400	MYLEGNADSALS
DR4	455	IYLEDGTGSAVSLE

Fig. 2

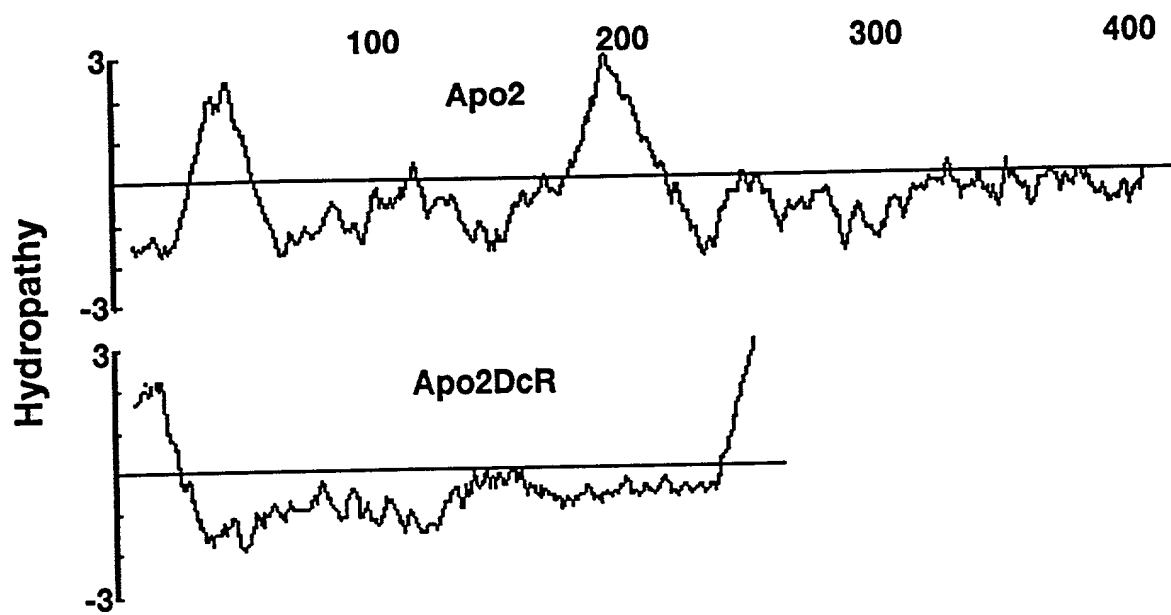


Figure 3

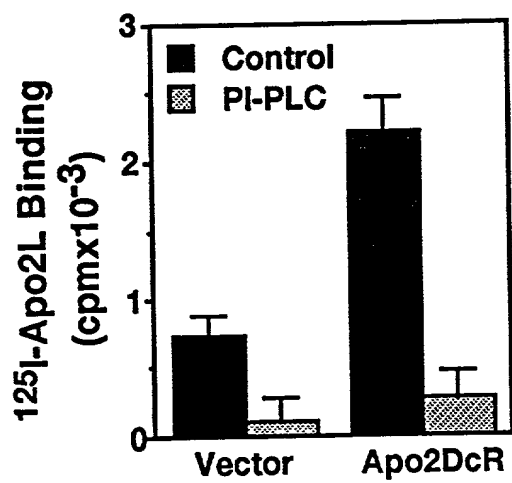


Figure 4

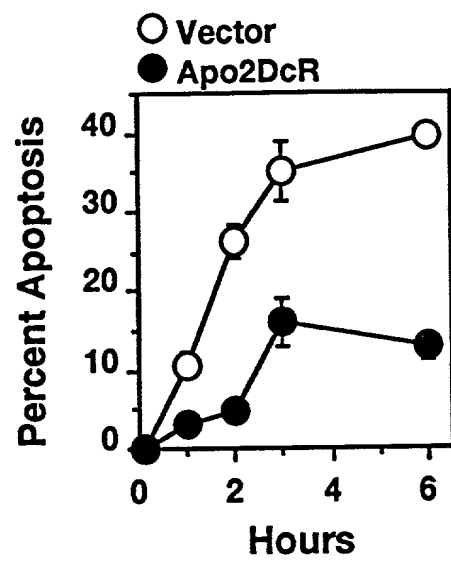


Figure 5

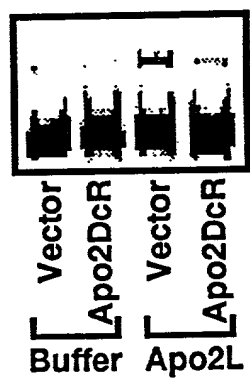


Figure 6

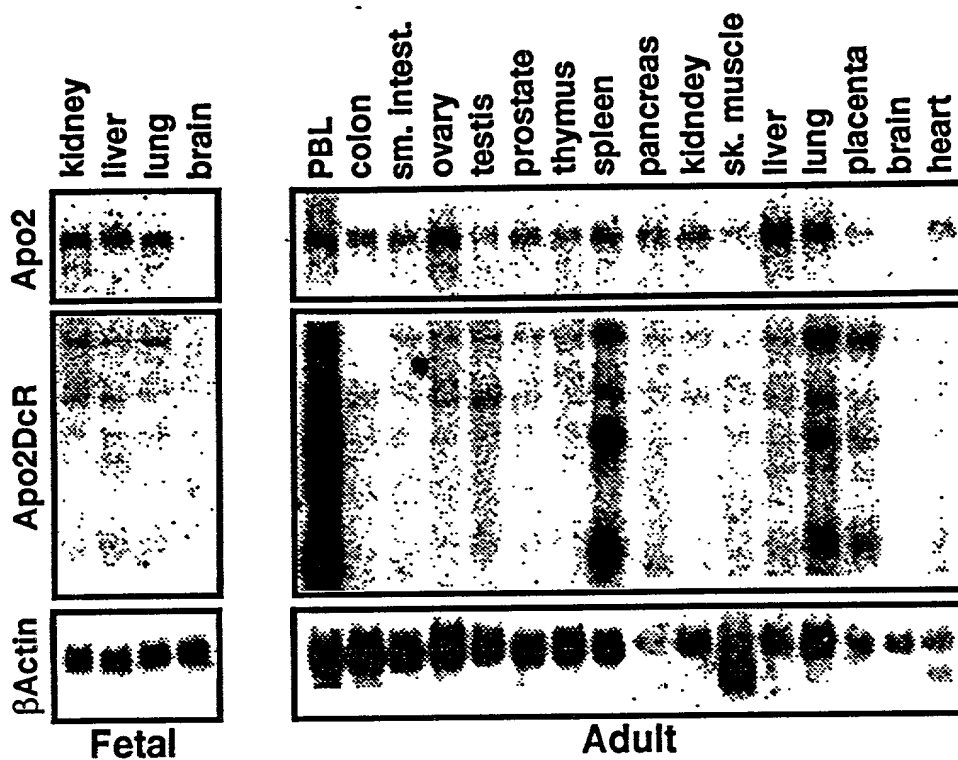


Figure 7



1 CCCACGGCGTC CGCATAAATC AGCAGCGCGC CGGAGAAACC CGCAATCTCT GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC  
 GGGTGCGCAG CGGTATTTAG TCGTGCGCGC GCCTCTGGG CGGTAGAGA CGCGGTGCT TTAATGGCT GCTACGGCT AGATGAAATT CCGACTTTG

101 CCACGGGCGCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGAACAACG GGGACAGAC GCCCGGGCG CTTCGGGGG CCGAAAAGG CACGGCCCCAG  
 GGTGCCCGGA CTCCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTG CCTGTCTTG CCGGGCGGG GAAGCCCCG GGCCTTTTCC GTGCCGGGTC

1 M etGluGlnar gGlyGlnasn AlaProAla laSerGlyAl aArgLysArg HisGlyProGly

201 GACCCAGGA GGGCGGGGA GCCAGGCCTG GGTCCGGGT CCCAAGACC CTTGTGCTCG TTGTGCGCG GTCTCTGCTG TTGGTCTCAG CTGAGTCTGC  
 CTGGGTCCCT CCGGCCCTT CCGTCCGAC CCGAGGCCA GGGTTCTGG GAACAGGCG AACAGCGCG CCAGGACGAC AACCAGAGTC GACTCAGACG

22 ProArgG1 uAlaArgGly AlaArgProG AlaArgProG lLeuArgVa lProLysThr LeuValLeu alValAlaAl aValLeuLeu LeuValserA laGluSerAla

301 TCTGATCACC CAACAAGACC TAGTCCCCA TAGTCCCCA GCAGAGAGCG GCCCACAAAC AAAAGAGGTC CAGCCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC  
 AGACTAGTGG GTTGTCTTGG ATCAGGGGT CGTCTCTGC CGGGTGTG TTTTCTCCAG GTCGGGGAGT CTCCCTAACA CAGGTGGACC TGTGGTATAG

55 LeuileThr GlnGlnAspL euAlaProG1 nGlnArgAla AlaProGlnG InLysArgse rSerProser GluGlyLeuC ysProProG1 yHisHisIle

401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT  
 AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CCGCAGCTGG TCCACACTAA

88 SerGluaspG lyArgAspCy sIleSerCys LysTyrglyG InaspTyrse rThrHisTrp AsnAspLeuL eupheCysLe uArgCysThr ArgCysAspSer

501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CCAGCAGAA CACAGTGTGT CAGTGCAGG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCCG  
 GTCCACTTCA CCTCGATTCA GGGAGTGGT GGTGGTCTTT GTGTACACA GTACAGCTTC TTCCGTGGAA GGCCTTCTT CTAAGAGGAC TCTACACGGC

122 GlyGluVa lGluLeuser ProCysThrT hrThrArgas nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspserProG lumetCysArg

601 GAAGTGCCGC ACAGGGTGT CCAGAGGGAT GGTCAAAGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA  
 CTTACAGGCG TGTCCACAG GGTCTCCCTA CCAGTTCAG CCACTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT

155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCyst hrProTrpse rAspIleGlu CysValHisL ysGluSerG1 yIleIleIle

701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGGAAAGAAAG TCCTTCTCTTA CCTGAAAGGC ATCTGCTCAG  
 CCTCAGTGT ACCTGCGCA TCAGAACTAA CACCGACACA CACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC

188 GlyValThrV alAlaAlaVa lValLeuIle ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alleuProTy rLeuLysGly IleCysSerGly

801 GTGGTGGTGG GGACCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCTCTCAA TGAGATCGTG AGTATCTTGC AGCCCCACA  
 CACCACCAAC CCTGGGACTC GCACACCTGT CTTGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT

222 GlyGlyG1 yAspProGlu ArgValaspA rgSerSerG1 nArgProGly AlaGluAspa snValLeuAs nGluIleVal serIleLeuG InProThrGln

901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA  
 CCAGGGACTC GTCCTTTACC TTCAGGTCTT CCGTGTCTC GGTGTCCAC AGTTGTACAA CAGGGGGGCC CTGAGTCTCG TAGACGACCT TGGCCGCTCTT

255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alAsnMetLe userProGly GluSerGluH isLeuLeuG1 uProAlaGlu

1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC  
 CGACTTTCCA GAGTCTCCTC CTCGACGAC CAAGGTCTGT TACTTCCACT AGGGTGACTC TGAGACTCTG TCACGAAGCT ACTGAAACGT CTGAACCCAG

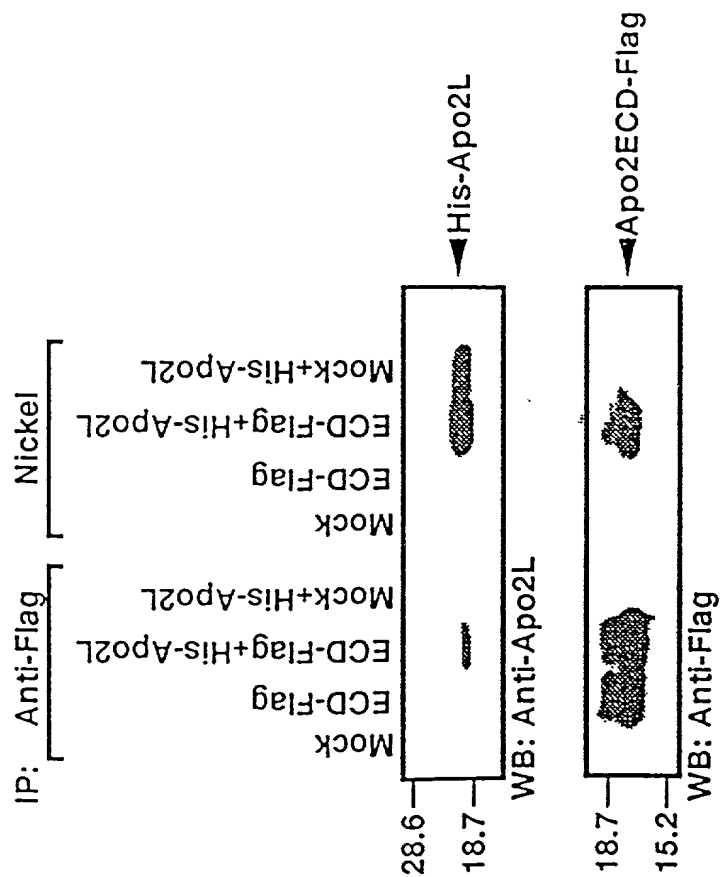
288 AlaGluuArg sArgGlnArgar gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG InCysPheAs pasPheAla AspLeuValPro

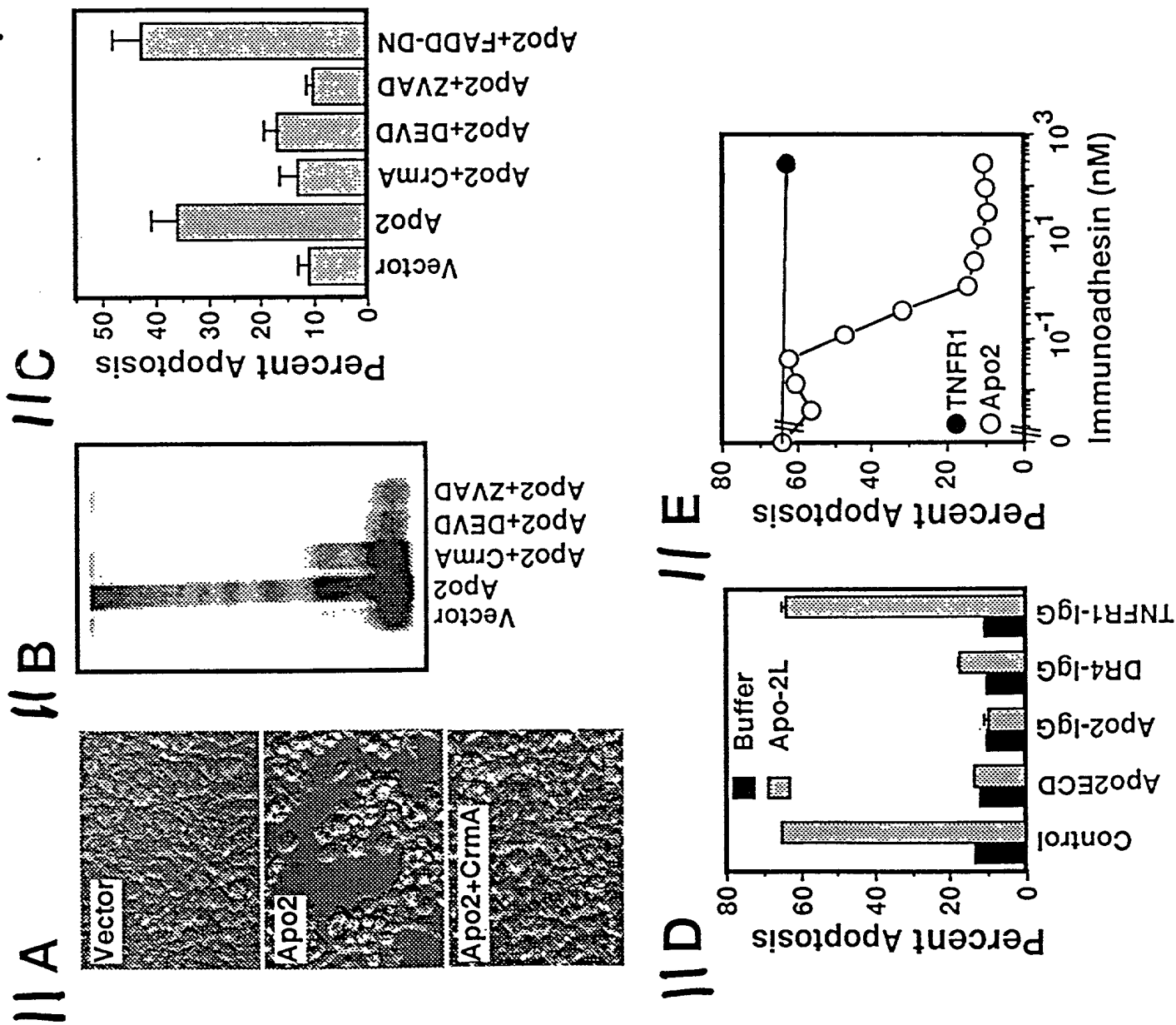
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GGAAACTGAG GACCCCTCGG GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCATTTTCC ACCGATTTCG ACTCCGTCGC CCGGTGTCCC TGTGGAACAT  
322 PheAspse rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysv alalaLysAl aGluAlaAla GlyHisArgA spThrLeuTyx  
1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCTTGCT GGATGCCCTG GAGACGCTGG GAGAGAGACT TGCCAAAGCAG  
GTGCTACGAC TATTTCAACC AGTTGTTTGG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGTTTCGTC  
355 ThrMetLeu ileLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln  
1301 AAGATTGAGG ACCACTTGTG GAGCTCTGGA AAGTTCATGT ATCTAGAAAG TAATGCAGAC TCTGCCWGTG CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA  
TTCTAACTCC TGGTGAAACA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGCTCG AGACGGRAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT  
388 LysilleGlua spHisLeuLe userSerGly LysPheMetT yrLeuGluGl yAsnAlaasp SerAlaXqq S erOC\*  
1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AAGACCTTTT TCGGGTTGAC GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC  
GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCCTTC ACGGTGTTAA CAGTGACTG GCCATGACCT TCTTTGAGAG  
1501 CCATCCAAAC TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT  
GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTGC ACTTACACTA TTATTCTCTGT GATACCTTTA  
1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTGT TGGGATGTCA TTGTTTTTCAC AGCAGTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT  
CAGACCTAGT AAGGCAAAAC CGCATGAAAC TCFAAACCAA ACCCTACAGT AACAAAAAGTG TCGTGAAAAA ATAGGATTAC ATTTACGAAA TAAATAAATA  
1701 TTGGGGTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAA GCGGCGCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC  
AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCGGCGCG TGAGATCTCA GCTGGACGTC TTCGAACCGG CCGTACCGG

Fig. 8 (cont.)

FIG. 9

1 MEORGONAPAAAGARKRHGPGPREARGARPGLRVPTLLVVAALLLVSAESALITQQD  
61 LAPQORAAFPQQRSSPSEGLCPGHHISEDGRDCISCKYGQDYSTHWNDDLFCRLRCTRCD  
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRGTGCPRGMVKVGDCPTPWSDI~~ECVH~~  
181 ~~KESGIIIGVTVA~~AVVLI~~VAVFVCKSL~~WKKVLPYLK~~ICSGGGGDP~~ERVDRSSQRRP~~GAED~~  
241 NVLNEIVSILQPTQVPEQEMEVEQEPAP~~EPTGVNMLSP~~GESEHLLLEPAEAERSQRRRLVPA  
301 NEGDPTETLRQCFDDFADIVPFD~~SWEPIMRK~~LGMDNEIKVAKAEAA~~GHRD~~TLYTMLIKW  
361 ~~VNKTGRDASVHTLLDALET~~GERLAKQK~~IEDHLLSSGK~~FMYLEGNADSALS





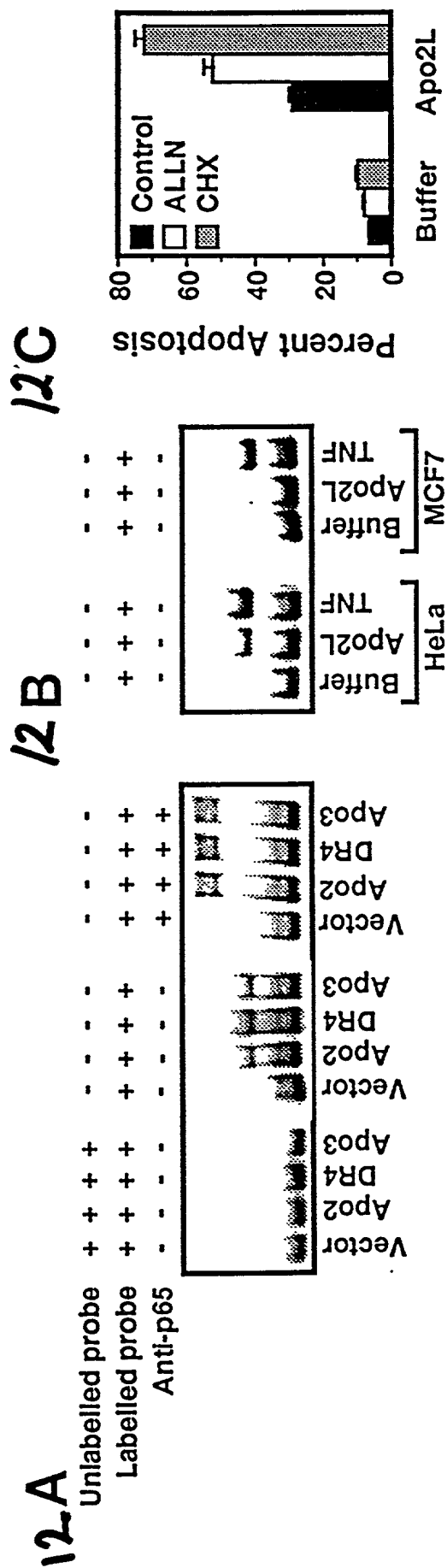


Fig. 12

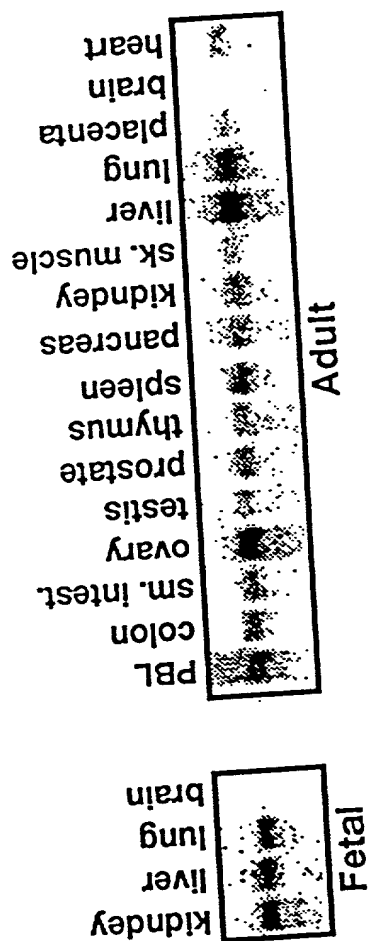


FIG. 13